

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Harris, Curtis C.  
Wang, Xin Wei  
Hoeijmakers, Jan H.J.
- (ii) TITLE OF INVENTION: Screening Assays for Compounds That Cause Apoptosis
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Townsend and Townsend and Crew LLP
  - (B) STREET: Two Embarcadero Center, Eighth Floor
  - (C) CITY: San Francisco
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/359,316
  - (B) FILING DATE: 19-DEC-1994
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Weber, Kenneth A.
  - (B) REGISTRATION NUMBER: 31,677
  - (C) REFERENCE/DOCKET NUMBER: 15280-225000
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (415) 576-0200
  - (B) TELEFAX: (415) 576-0300

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 393 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..393
  - (D) OTHER INFORMATION: /note= "human wild-type p53"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Glu	Glu	Pro	Gln	Ser	Asp	Pro	Ser	Val	Glu	Pro	Pro	Leu	Ser	Gln	1	5	10	15
Glu	Thr	Phe	Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro	Glu	Asn	Asn	Val	Leu	20	25	30	
Ser	Pro	Leu	Pro	Ser	Gln	Ala	Met	Asp	Asp	Leu	Met	Leu	Ser	Pro	Asp	35	40	45	
Asp	Ile	Glu	Gln	Trp	Phe	Thr	Glu	Asp	Pro	Gly	Pro	Asp	Glu	Ala	Pro	50	55	60	
Arg	Met	Pro	Glu	Ala	Ala	Pro	Arg	Val	Ala	Pro	Gly	Pro	Ala	Ala	Pro	65	70	75	
Thr	Pro	Ala	Ala	Pro	Ala	Pro	Ala	Pro	Ser	Trp	Pro	Leu	Ser	Ser	Ser	85	90	95	
Val	Pro	Ser	Gln	Lys	Thr	Tyr	Gln	Gly	Ser	Tyr	Gly	Phe	Arg	Leu	Gly	100	105	110	
Phe	Leu	His	Ser	Gly	Thr	Ala	Lys	Ser	Val	Thr	Cys	Thr	Tyr	Ser	Pro	115	120	125	
Ala	Leu	Asn	Lys	Met	Phe	Cys	Gln	Leu	Ala	Lys	Thr	Cys	Pro	Val	Gln	130	135	140	
Leu	Trp	Val	Asp	Ser	Thr	Pro	Pro	Pro	Gly	Thr	Arg	Val	Arg	Ala	Met	145	150	155	
Ala	Ile	Tyr	Lys	Gln	Ser	Gln	His	Met	Thr	Glu	Val	Val	Arg	Arg	Cys	165	170	175	
Pro	His	His	Glu	Arg	Cys	Ser	Asp	Ser	Asp	Gly	Leu	Ala	Pro	Pro	Gln	180	185	190	
His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Leu	Arg	Val	Glu	Tyr	Leu	Asp	Asp	195	200	205	
Arg	Asn	Thr	Phe	Arg	His	Ser	Val	Val	Val	Pro	Tyr	Glu	Pro	Pro	Glu	210	215	220	
Val	Gly	Ser	Asp	Cys	Thr	Thr	Ile	His	Tyr	Asn	Tyr	Met	Cys	Asn	Ser	225	230	235	
Ser	Cys	Met	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Thr	Ile	Ile	Thr	245	250	255	
Leu	Glu	Asp	Ser	Ser	Gly	Asn	Leu	Leu	Gly	Arg	Asn	Ser	Phe	Glu	Val	260	265	270	
Arg	Val	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Arg	Thr	Glu	Glu	Glu	Asn	275	280	285	
Leu	Arg	Lys	Lys	Gly	Glu	Pro	His	His	Glu	Leu	Pro	Pro	Gly	Ser	Thr	290	295	300	
Lys	Arg	Ala	Leu	Pro	Asn	Asn	Thr	Ser	Ser	Ser	Pro	Gln	Pro	Lys	Lys	305	310	315	
Lys	Pro	Leu	Asp	Gly	Glu	Tyr	Phe	Thr	Leu	Gln	Ile	Arg	Gly	Arg	Glu	325	330	335	
Arg	Phe	Glu	Met	Phe	Arg	Glu	Leu	Asn	Glu	Ala	Leu	Glu	Leu	Lys	Asp	340	345	350	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..21  
(D) OTHER INFORMATION: /note= "peptide # p53cp from amino acid residues 367-387 of human wild-type p53 capable of inhibiting binding of wild-type p53 to XPB"

Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys  
1 5 10 15  
Leu Met Phe Lys Thr  
20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 781 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Protein  
(B) LOCATION: 1..781  
(D) OTHER INFORMATION: /note= "human xeroderma pigmentosum B (XPB) helicase protein"

Met	Gly	Lys	Arg	Asp	Arg	Ala	Asp	Arg	Asp	Lys	Lys	Lys	Ser	Arg	Lys
1				5					10					15	
Arg	His	Tyr	Glu	Asp	Glu	Glu	Asp	Asp	Glu	Glu	Asp	Ala	Pro	Gly	Asn
			20					25					30		
Asp	Pro	Gln	Glu	Ala	Val	Pro	Ser	Ala	Ala	Gly	Lys	Gln	Val	Asp	Glu
		35					40					45			

Ser Gly Thr Lys Val Asp Glu Tyr Gly Ala Lys Asp Tyr Arg Leu Gln  
 50 55 60  
 Met Pro Leu Lys Asp Asp His Thr Ser Arg Pro Leu Trp Val Ala Pro  
 65 70 75 80  
 Asp Gly His Ile Phe Leu Glu Ala Phe Ser Pro Val Tyr Lys Tyr Ala  
 85 90 95  
 Gln Asp Phe Leu Val Ala Ile Ala Glu Pro Val Cys Arg Pro Thr His  
 100 105 110  
 Val His Glu Tyr Lys Leu Thr Ala Tyr Ser Leu Tyr Ala Ala Val Ser  
 115 120 125  
 Val Gly Leu Gln Thr Ser Asp Ile Thr Glu Tyr Leu Arg Lys Leu Ser  
 130 135 140  
 Lys Thr Gly Val Pro Asp Gly Ile Met Gln Phe Ile Lys Leu Cys Thr  
 145 150 155 160  
 Val Ser Tyr Gly Lys Val Lys Leu Val Leu Lys His Asn Arg Tyr Phe  
 165 170 175  
 Val Glu Ser Cys His Pro Asp Val Ile Gln His Leu Leu Gln Asp Pro  
 180 185 190  
 Val Ile Arg Glu Cys Arg Leu Arg Asn Ser Glu Gly Glu Ala Thr Glu  
 195 200 205  
 Leu Ile Thr Glu Thr Phe Thr Ser Lys Ser Ala Ile Ser Lys Thr Ala  
 210 215 220  
 Glu Ser Ser Gly Gly Pro Ser Thr Ser Arg Val Thr Asp Pro Gln Gly  
 225 230 235 240  
 Lys Ser Asp Ile Pro Met Asp Leu Phe Asp Phe Tyr Glu Gln Met Asp  
 245 250 255  
 Lys Asp Glu Glu Glu Glu Glu Thr Gln Thr Val Ser Phe Glu Val  
 260 265 270  
 Lys Gln Glu Met Ile Glu Glu Leu Gln Lys Arg Cys Ile His Leu Glu  
 275 280 285  
 Tyr Pro Leu Leu Ala Glu Tyr Asp Phe Arg Asn Asp Ser Val Asn Pro  
 290 295 300  
 Asp Ile Asn Ile Asp Leu Lys Pro Thr Ala Val Leu Arg Pro Tyr Gln  
 305 310 315 320  
 Glu Lys Ser Leu Arg Lys Met Phe Gly Asn Gly Arg Ala Arg Ser Gly  
 325 330 335  
 Val Ile Val Leu Pro Cys Gly Ala Gly Lys Ser Leu Val Gly Val Thr  
 340 345 350  
 Ala Ala Cys Thr Val Arg Lys Arg Cys Leu Val Leu Gly Asn Ser Ala  
 355 360 365  
 Val Ser Val Glu Gln Trp Lys Ala Gln Phe Lys Met Trp Ser Thr Ile  
 370 375 380  
 Asp Asp Ser Gln Ile Cys Arg Phe Thr Ser Asp Ala Lys Asp Lys Pro  
 385 390 395 400

Ile Gly Cys Ser Val Ala Ile Ser Thr Tyr Ser Met Leu Gly His Thr  
 405 410 415  
 Thr Lys Arg Ser Trp Glu Ala Glu Arg Val Met Glu Trp Leu Lys Thr  
 420 425 430  
 Gln Glu Trp Gly Leu Met Ile Leu Asp Glu Val His Thr Ile Pro Ala  
 435 440 445  
 Lys Met Phe Arg Arg Val Leu Thr Ile Val Gln Ala His Cys Lys Leu  
 450 455 460  
 Gly Leu Thr Ala Thr Leu Val Arg Glu Asp Asp Lys Ile Val Asp Leu  
 465 470 475 480  
 Asn Phe Leu Ile Gly Pro Lys Leu Tyr Glu Ala Asn Trp Met Glu Leu  
 485 490 495  
 Gln Asn Asn Gly Tyr Ile Ala Lys Val Gln Cys Ala Glu Val Trp Cys  
 500 505 510  
 Pro Met Ser Pro Glu Phe Tyr Arg Glu Tyr Val Ala Ile Lys Thr Lys  
 515 520 525  
 Lys Arg Ile Leu Leu Tyr Thr Met Asn Pro Asn Lys Phe Arg Ala Cys  
 530 535 540  
 Gln Phe Leu Ile Lys Phe His Glu Arg Arg Asn Asp Lys Ile Ile Val  
 545 550 555 560  
 Phe Ala Asp Asn Val Phe Ala Leu Lys Glu Tyr Ala Ile Arg Leu Asn  
 565 570 575  
 Lys Pro Tyr Ile Tyr Gly Pro Thr Ser Gln Gly Glu Arg Met Gln Ile  
 580 585 590  
 Leu Gln Asn Phe Lys His Asn Pro Lys Ile Asn Thr Ile Phe Ile Ser  
 595 600 605  
 Lys Val Gly Asp Thr Ser Phe Asp Leu Pro Glu Ala Asn Val Leu Ile  
 610 615 620  
 Gln Ile Ser Ser His Gly Gly Ser Arg Arg Gln Glu Ala Gln Arg Leu  
 625 630 635 640  
 Gly Arg Val Leu Arg Ala Lys Lys Gly Met Val Ala Glu Glu Tyr Asn  
 645 650 655  
 Ala Phe Phe Tyr Ser Leu Val Ser Gln Asp Thr Gln Glu Met Ala Tyr  
 660 665 670  
 Ser Thr Lys Arg Gln Arg Phe Leu Val Gln Gly Tyr Ser Phe Lys Val  
 675 680 685  
 Ile Thr Lys Leu Ala Gly Met Glu Glu Glu Asp Leu Ala Phe Ser Thr  
 690 695 700  
 Lys Glu Glu Gln Gln Gln Leu Leu Gln Lys Val Leu Ala Ala Thr Asp  
 705 710 715 720  
 Leu Asp Ala Glu Glu Glu Val Val Ala Gly Glu Phe Gly Ser Arg Ser  
 725 730 735  
 Ser Gln Ala Ser Arg Arg Phe Gly Thr Met Ser Ser Met Ser Gly Ala  
 740 745 750

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 15 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
    (A) NAME/KEY: Peptide
    (B) LOCATION: 1..15
    (D) OTHER INFORMATION: /note= "peptide # 464 from amino acid
                             residues 464-478 of the helicase III
                             region of XPB protein capable of
                             inhibiting binding of wild-type p53
                             to XPB"
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Leu Gly Leu Thr Ala Thr Leu Val Arg Glu Asp Asp Lys Ile Val  
1 5 10 15

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 15 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
    (A) NAME/KEY: Peptide
    (B) LOCATION: 1..15
    (D) OTHER INFORMATION: /note= "peptide # 479 from amino acid
                           residues 479-493 of XPB protein
                           incapable of inhibiting binding of
                           wild-type p53 to XPB"
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Asp Leu Asn Phe Leu Ile Gly Pro Lys Leu Tyr Glu Ala Asn Trp  
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /note= "peptide # 99 irrelevant peptide  
from HBV"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly	Leu	Ser	Ala	Met	Ser	Thr	Thr	Asp	Leu	Glu	Ala	Tyr	Phe	Lys	Asp
1				5					10					15	